

SEQUENCE LISTING

<110> Richardson, Alan E.
Hayes, Julie E.
Simpson, Richard J.

<120> Expression of phytase in plants
as a method of modifying plant productivity

<130> 37-02

<140> US 10/089,364

<141> 2002-03-25

<150> PCT/AU00/01183

<151> 2000-09-23

<150> AU PQ3049

<151> 1999-09-24

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<170> PatentIn Ver. 2.0

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 Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr Thr Phe Glu Gly Lys Tyr
 115 120 125
 Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr
 130 135 140
 Pro Phe Gly Glu Gln Glu Leu Val Asn Ser Gly Val Lys Phe Tyr Gln
 145 150 155 160
 Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val Pro Phe Ile Arg Ser Ser
 165 170 175
 Gly Ser Asn Arg Val Ile Ala Ser Gly Asn Lys Phe Ile Glu Gly Phe
 180 185 190
 Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser
 195 200 205
 Pro Lys Ile Asp Val Val Ile Ser Glu Ala Ser Thr Ser Asn Asn Thr
 210 215 220

Leu Asp Pro Gly Thr Cys Thr Val Phe Glu Asp Ser Glu Leu Ala Asp
 225 230 235 240
 Asp Ile Glu Ala Asn Phe Thr Ala Thr Phe Val Pro Ser Ile Arg Gln
 245 250 255
 Arg Leu Glu Asn Asp Leu Ser Gly Val Ser Leu Thr Asp Thr Glu Val
 260 265 270
 Thr Tyr Leu Met Asp Met Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr
 275 280 285
 Val Asp Thr Lys Leu Ser Pro Phe Cys Asp Leu Phe Thr His Glu Glu
 290 295 300
 Trp Ile Asn Tyr Asp Tyr Leu Gln Ser Pro Asn Lys Tyr Tyr Gly His
 305 310 315 320
 Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn
 325 330 335
 Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr Ser
 340 345 350
 Ser Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ser
 355 360 365
 Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile Leu
 370 375 380
 Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Ser Thr Thr
 385 390 395 400
 Ala Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr Val
 405 410 415
 Pro Phe Ala Ser Arg Met Tyr Val Glu Met Met Gln Cys Gln Ser Glu
 420 425 430
 Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu
 435 440 445
 His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe
 450 455 460
 Val Lys Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys
 465 470 475 480

Phe Ala

<210> 11

<211> 1449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimeric
 ext::phyA-1 gene

<220>

<221> CDS

<222> (1)..(1446)

<400> 11

atg gga aga att gct aga ggc tca aaa atg agt tct ctc att gtg tct	48
Met Gly Arg Ile Ala Arg Gly Ser Lys Met Ser Ser Leu Ile Val Ser	
1 5 10 15	
ttg ctt gta gta ttg gtg tca ctc aat ttg gct tcc gaa acc aca gct	96
Leu Leu Val Leu Val Ser Leu Asn Leu Ala Ser Glu Thr Thr Ala	
20 25 30	
gcc atg ctg gca gtc ccc gcc tcg aga aat caa tcc agt tgc gat acg	144
Ala Met Leu Ala Val Pro Ala Ser Arg Asn Gln Ser Ser Cys Asp Thr	
35 40 45	
gtc gat cag ggg tat caa tgc ttc tcc gag act tcg cat ctt tgg ggt	192
Val Asp Gln Gly Tyr Gln Cys Phe Ser Glu Thr Ser His Leu Trp Gly	
50 55 60	
caa tac gca ccg ttc ttc tct ctg gca aac gaa tcg gtc atc tcc cct	240
Gln Tyr Ala Pro Phe Phe Ser Leu Ala Asn Glu Ser Val Ile Ser Pro	
65 70 75 80	
gag gtg ccc gcc gga tgc aga gtc act ttc gct cag gtc ctc tcc cgt	288
Glu Val Pro Ala Gly Cys Arg Val Thr Phe Ala Gln Val Leu Ser Arg	
85 90 95	
cat gga gcg cgg tat ccg acc gac tcc aag ggc aag aaa tac tcc gct	336
His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala	
100 105 110	
ctc att gag gag atc cag cag aac gcg acc acc ttt gac gga aaa tat	384
Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr Thr Phe Asp Gly Lys Tyr	
115 120 125	
gcc ttc ctg aag aca tac aac tac agc ttg ggt gca gat gac ctg act	432
Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr	
130 135 140	
ccc ttc gga gaa cag gag cta gtc aac tcc ggc atc aag ttc tac cag	480
Pro Phe Gly Glu Gln Glu Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln	
145 150 155 160	
cgg tac gaa tcg ctc aca agg aac atc gtt cca ttc atc cga tcc tct	528
Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val Pro Phe Ile Arg Ser Ser	
165 170 175	
ggc tcc agc cgc gtg atc gcc tcc ggc aag aaa ttc atc gag ggc ttc	576
Gly Ser Ser Arg Val Ile Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe	
180 185 190	
cag agc acc aag ctg aag gat cct cgt gcc cag ccc ggc caa tcg tcg	624
Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser	
195 200 205	
ccc aag atc gac gtg gtc att tcc gag gcc agc tca tcc aac aac act	672
Pro Lys Ile Asp Val Val Ile Ser Glu Ala Ser Ser Ser Asn Asn Thr	
210 215 220	

15

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gtg agg ggg ttg agc ttt gct aga tct ggg ggt gat tgg gcg gag tgt 1440
Val Arg Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys
465                               470                               475                               480

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ttt gct tag 1449
Phe Ala

```

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<210> 12
<211> 482
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: chimeric ext::phyA-1 gene

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<400> 12
Met Gly Arg Ile Ala Arg Gly Ser Lys Met Ser Ser Leu Ile Val Ser
  1                               5                               10                               15

Leu Leu Val Val Leu Val Ser Leu Asn Leu Ala Ser Glu Thr Thr Ala
      20                               25                               30

Ala Met Leu Ala Val Pro Ala Ser Arg Asn Gln Ser Ser Cys Asp Thr
      35                               40                               45

Val Asp Gln Gly Tyr Gln Cys Phe Ser Glu Thr Ser His Leu Trp Gly
      50                               55                               60

Gln Tyr Ala Pro Phe Phe Ser Leu Ala Asn Glu Ser Val Ile Ser Pro
      65                               70                               75                               80

Glu Val Pro Ala Gly Cys Arg Val Thr Phe Ala Gln Val Leu Ser Arg
      85                               90                               95

His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala
      100                               105                               110

Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr Thr Phe Asp Gly Lys Tyr
      115                               120                               125

Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr
      130                               135                               140

Pro Phe Gly Glu Gln Glu Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln
      145                               150                               155                               160

Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val Pro Phe Ile Arg Ser Ser
      165                               170                               175

Gly Ser Ser Arg Val Ile Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe
      180                               185                               190

Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser
      195                               200                               205

Pro Lys Ile Asp Val Val Ile Ser Glu Ala Ser Ser Ser Asn Asn Thr
      210                               215                               220

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Leu Asp Pro Gly Thr Cys Thr Val Phe Glu Asp Ser Glu Leu Ala Asp
225                               230                235                240

Thr Val Glu Ala Asn Phe Thr Ala Thr Phe Val Pro Ser Ile Arg Gln
                               245                250                255

Arg Leu Glu Asn Asp Leu Ser Gly Val Thr Leu Thr Asp Thr Glu Val
                               260                265                270

Thr Tyr Leu Met Asp Met Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr
                275                               280                285

Val Asp Thr Lys Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp Glu
                290                               295                300

Trp Ile Asn Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly His
305                               310                315                320

Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn
                               325                330                335

Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr Ser
                340                               345                350

Ser Asn His Thr Leu Asp Ser Ser Pro Ala Thr Phe Pro Leu Asn Ser
                355                               360                365

Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile Leu
370                               375                380

Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr Thr
385                               390                395                400

Val Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr Val
                405                               410                415

Pro Phe Ala Ser Arg Leu Tyr Val Glu Met Met Gln Cys Gln Ala Glu
                420                               425                430

Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu
                435                               440                445

His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe
                450                               455                460

Val Arg Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys
465                               470                475                480

Phe Ala

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<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13
 cgcggaattca tgctggcagt ccccgctcgc 30

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 14
 ggcacgcgac taagcaaaac actccgc 27

<210> 15
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 15
 gcgtctagag aattcatggg aagaattgct ag 32

<210> 16
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 16
 cgcggaacccg cgcccgacgc tgtgggttcg gaagc 35

<210> 17
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ext::phytase
 junction

<400> 17
 acgctgccat gctggca 17

<210> 18
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ext::phytase
 junction

<400> 18
Thr Ala Ala Met Leu Ala
1 5
18